

SEQUENCE LISTING

<110> Conaris Research Institute GmbH

<120> Diagnostic Use of Polymorphisms in the Gene Coding for
the TNF Receptor II and Method for Detecting
Non-Responders to Anti-TNF-Therapy

<130> K51347/8

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<170> PatentIn Ver. 2:1

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<210> 41

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<223> Description of Artificial Sequence: FAM Probe

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Met Ala Pro Val Ala Val Trp Ala
-20 -15

gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
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Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
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Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
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tgc tgc ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tgc gac 305
 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
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acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
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tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401
 Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
 70 75 80

gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc 449
 Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
 85 90 95

agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg 497
 Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu
 100 105 110

tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca 545
 Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro
 115 120 125 130

gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg 593
 Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
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ttc tcc aac acg act tca tcc acg gat att tgc agg ccc cac cag atc 641
 Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile
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tgt aac gtg gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc 689
 Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys
 165 170 175

acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta 737
 Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu
 180 185 190

ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa 785
 Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu
 195 200 205 210

ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc 833
 Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser
 215 220 225

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Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
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tgt	gtc	atc	atg	acc	cag	gtg	aaa	aag	aag	ccc	ttg	tgc	ctg	cag	aga	977
Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
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gaa	gcc	aag	gtg	cct	cac	ttg	cct	gcc	gat	aag	gcc	cgg	ggt	aca	cag	1025
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Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
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Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	
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His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	
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gat	tcc	agc	ccc	tcg	gag	tcc	cgg	aag	gac	gag	cag	gtc	ccc	ttc	tcc	1361
Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	
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aag	gag	gaa	tgt	gcc	ttt	cgg	tca	cag	ctg	gag	acg	cca	gag	acc	ctg	1409
Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	
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 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
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 Gly Met Lys Pro Ser
 435 440

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Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr
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Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly
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	275						280					285			
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305					310					315					320
Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser
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Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln
385					390						395				400
Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro
				405					410					415	
Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser
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 Met Ala Pro Val Ala Val Trp Ala
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 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
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 gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc 209
 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
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 Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
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 tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
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 acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
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Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
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gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc 449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
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agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc cgg ctg 497
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu
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tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc aga cca 545
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro
115 120 125 130

gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg ggg acg 593
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
135 140 145

ttc tcc aac acg act tca tcc acg gat att tgc agg ccc cac cag atc 641
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile
150 155 160

tgt aac gtg gtg gcc atc cct ggg aat gca agc atg gat gca gtc tgc 689
Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys
165 170 175

acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta 737
Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu
180 185 190

ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa 785
Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu
195 200 205 210

ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc ccc agc 833
Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser
215 220 225

ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca gtt gga ctg 881
Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu
230 235 240

att gtg ggt gtg aca gcc ttg ggt cta cta ata ata gga gtg gtg aac 929
Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn
245 250 255

tgt gtc atc atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga 977

'Cys' Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg
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gaa gcc aag gtg cct cac ttg cct gcc gat aag gcc cgg ggt aca cag 1025
 Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln
 275 280 285 290

ggc ccc gag cag cag cac ctg ctg atc aca gcg ccg agc tcc agc agc 1073
 Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser
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agc tcc ctg gag agc tcg gcc agt gcg ttg gac aga agg gcg ccc act 1121
 Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr
 310 315 320

cgg aac cag cca cag gca cca ggc gtg gag gcc agt ggg gcc ggg gag 1169
 Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
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gcc cgg gcc agc acc ggg agc tca gat tct tcc cct ggt gcc cat ggg 1217
 Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly
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acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac 1265
 Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp
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cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca 1313
 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
 375 380 385

gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc 1361
 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
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aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca gag acc ctg 1409
 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
 405 410 415

ctg ggg agc acc gaa gag aag ccc ctg ccc ctt gga gtg cct gat gct 1457
 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
 420 425 430

ggg atg aag ccc agt taa ccaggccggt gtgggctgtg tcgtagccaa 1505
 Gly Met Lys Pro Ser
 435 440

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 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
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 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
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Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
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 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
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<222> (90)..(1475)

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Met Ala Pro Val Ala Val Trp Ala
-20 -15

gcg ctg gcc gtc gga ctg gag ctc tgg gct gcg gcg cac gcc ttg ccc 161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
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Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
5 10 15

cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aag 257
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
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tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc tcg gac 305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
35 40 45 50

acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc tgg aac 353
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
55 60 65

tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag 401
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
70 75 80

gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc 449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
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Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	
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Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr	
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Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile	
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Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu	
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ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa	785
Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr Pro Glu	
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Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly Pro Ser	
215 220 225	
ccc cca gct gaa ggg agc act ggc gac ttc gct ctt cca gtt gga ctg	881
Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly Leu	
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Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn	
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Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg	
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gaa gcc aag gtg cct cac ttg cct gcc gat aag gcc cgg ggt aca cag	1025
Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln	
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ggc ccc gag cag cag cac ctg ctg atc aca gcg ccg agc tcc agc agc	1073
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 Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr
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 Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
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cac agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca 1313
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 375 380 385

gat tcc agc ccc tcg gag tcc ccg aag gac gag cag gtc ccc ttc tcc 1361
 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
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 420 425 430

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 Gly Met Lys Pro Ser
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 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
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Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240
Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
245 250 255
Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
260 265 270
Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
275 280 285
Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
290 295 300
Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305 310 315 320
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
325 330 335
Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
340 345 350
Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
355 360 365
Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
370 375 380
Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385 390 395 400
Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
405 410 415
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
420 425 430
Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
435 440 445
Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
450 455 460